

```

AMSH1      THNKFTTHRVIP--KQSAGSDYCDMENVEKLNVDQDHD--LITLGNITPTQTAFLS
AMSH2      THNKFTTHRVIP--KQSAGSDYCDMENVEKLNVDQDHD--LITLGNITPTQTAFLS
AMSH       HANEFTTHRVIP--KQSAGSDYCDMENVEKLNVDQDHD--LITLGNITPTQTAFLS
Rpn11      TVRVIVDIAMRQS--GTVSVZAVDPTQAKMLDMLKQTGRPEHVSMLSCPSYGCNLS
Jab1       TMIIMDSIALFVSGTETRVNAQAAAAYTHGAYIENAKQVGRLENAIGWYSCPSYGCNLS
           . . . . .

AMSH1      SVLHHTCSYQIALPELAIVCSEKHKDTG-----IFRITNAGMLEVSACKKKGFH--PH
AMSH2      SVLHHTCSYQIALPELAIVCSEKHKDTG-----IFRITNAGMLEVSACKKKGFH--PH
AMSH       SVLHHTCSYQIALPELAIVCSEKHKDTG-----IFRITNAGMLEVSACKKKGFH--PH
Rpn11      GVDINTQCSFEALSKRAVAVVDPIQSVKGVVIDAFKLLNANWVVLGHEPQQTTSNLGR
Jab1       GIVVSTQMLNQOQFKPFVAVVIDPRTISAG----KVNIGATRTYPRGYKPPDEGFSKYQ
           . . . . .

AMSH1      TKPRPLFSICKHV--LVKDIXI-----IVLDR-----
AMSH2      TKPRPLFSICKHV--LVKDIXI-----IVLDR-----
AMSH       SKDPFLFCSCSHVT--VVDRAV-----ITDILR-----
Rpn11      LNKPSIQALINGLNRHYYSITINDRKNLEKQOMLNLNKKSNMKGITLQDYSEKCKNKS
Jab1       TIPLNKIIDFGVHCKQYXALEVSYFKSSILDRKLLLNKNYNVNTLSSSSLLTNADYTTG
           . . . . .

AMSH1      -----
AMSH2      L-----
AMSH       -----
Rpn11      VVKEMLELAKNKNRAXEKDKMTPQLAKNVGRQDKPRHLEKHVDVIMTSNIVQCLAM
Jab1       QVFDLSEKLEQSEALGRGSFMLG--LETRDRKSEDKLAKATRDSCKTTLEALINGLSPQV
           -----

AMSH1      -----
AMSH2      -----
AMSH       LDTVVVK-----
Rpn11      IKDKLFNQINIS
Jab1

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FIGURE 1



COP9\_bu5\_Ha VGRLENAIGWYHSHHPGYGCWLSGIDVSTQMLNQCFQEPFVA--VVIDPTRTISAGKVNLG  
 COP9\_bu5\_Dm VGRMEHAVGWYHSHHPGYGCWLSGINVSTQMLNQTYQEPFVA--IVVDPVRTVSAGKVCIG  
 COP9\_bu5\_At AGRLENVVVGWYHSHHPGYGCWLSGIDVSTQRLNQHQEPFLA--VVIDPTRTVSAGKVEIG  
 COP9\_bu5\_Co EGRKEKVVVGWYHSHHPGYGCWLSGIDVSTQTLNQKQEPFWA--IVIDPLRTMSAGKVDIG  
 AF2198\_Arcfu LPIGMKVFGTVHSHSPSCRPSEEDLSLFTLFGKYHIIVCY--PYDENSWKCYNRKGEEV  
 PH0451\_Pyrho MPHDESIGKGFHSHSPFPFPYSEGDLMFPSKFGGIHIIAFA--PYDEDSVKAFDSEGREV  
 TVN1035\_Thevo KPIDFSLVGSVHSHPSGITKPSDEDLRFMSLTGKIHIIVGY--PYNLKDYSAYDRSGREV  
 MTH971\_Metth LPPFTGAVGSVHSHPGPVNLPAAADLHFFSKNGLFHLIIAH--PYTMETVAAYTRNGDEV  
 aq\_1691\_Aquae ISKGMEIVGVYHSHPDHPRSQFDLQRAFPDLSYIIFSVQ--KGKVASYRSWELKGDKF  
 RV1334\_Myctu EDADAEVFPVVIYHSHATEAYPSRTDVKLATEPDAHYVLVSTRDPHRELSYRIVDGAFT  
 RadC\_Ecoli IKINASALILAHNHPSGCAEPSKADKLITERIIKSCQFMDL--RVLDHIVIGRGEYVSFA  
 .....HSHP.....S...D

FIGURE 3

|             |  |
|-------------|--|
| COP9_gu5_Hs | VGRLENAIGWYHSHPGYGCWLSGIDVSTQMLNQOFQEPFVA--VVIDPTRTISAGKVNIG |
| COP9_gu5_Dm | VGRMEHAVGWYHSHPGYGCWLSGINVSTQMLNOTYQEPFVA--IVVDPVRTVSAGKVCIG |
| COP9_gu5_At | AGRLNNVVGWYHSHPGYGCWLSGIDVSTQRLNQHQEPFLA--VVIDPRTVSAGKVBIG   |
| COP9_gu5_Ce | EGRKEKVVGWYHSHPGYGCWLSGIDVSTQTLNQKQEPWVA--IVIDPLRTMSAGKVDIG  |
| Pad1_Dm     | TGRPEMVGWYHSHPGFGCWLSGVDINTQSFQALSERAVA--VVVDPIQSVKG-KVVID   |
| Pad1_Hs     | TGRPEMVGWYHSHPGFGCWLSGVDINTQSFQALSERAVA--VVVDPIQSVKG-KVVID   |
| Skal_bd     | TGRDEIVIGWYHSHPGFGCWLSGVDINTQSFQALSRARA--VVVDPIQSVRG-KVVID   |
| Pad1_Sc     | TGRDQMVVGWYHSHPGFGCWLSGVDINTQKSFQALSRARA--VVVDPIQSVKG-KVVID  |
| .....       | HSIIP''''''S 'D  |

FIGURE 4